SEQUENCE LISTING

<110> HERMANN, Thomas WOLF, Andreas MORBACH, Susanne KRAMER, Reinhard <120> NUCLEOTIDE SEQUENCES CODING FOR THE OtsA PROTEIN <130> 215482US0X <150> DE 10103873.9 <151> 2001-01-30 <150> DE 10110760.9 <151> 2000-03-07 <160> ... <170> PatentIn version 3.1 <210> 7 <211> 3010 <212> DNA <213> Corynebacterium glutamicum <220> CDS <221> <222> (884)..(2338) <223> j, ЦŲ <400> 1 attgcggggc ttactgcgct gatgggttct gcgttttatt acctcttcgt tgtttattta 60 ggccccgtct ctgccgctgc gattgctgca acagcagttg gtttcactgg tggtttgctt 120 gcccgtcgat tcttgattcc accgttgatt gtggcgattg ccggcatcac accaatgctt 180 ccaggtctag caatttaccg cggaatgtac gccaccctga atgatcaaac actcatgggt 240 ttcaccaaca ttgcggttgc tttagccact gcttcatcac ttgccgctgg cgtggttttg 300 ggtgagtgga ttgcccgcag gctacgtcgt ccaccacgct tcaacccata ccgtgcattt 360 accaaggcga atgagttctc cttccaggag gaagctgagc agaatcagcg ccggcagaga 420 aaacgtccaa agactaatca gagattcggt aataaaaggt aaaaatcaac ctgcttaggc 480 gtctttcgct taaatagcgt agaatatcgg gtcgatcgct tttaaacact caggaggatc 540 cttgccggcc aaaatcacgg acactcgtcc caccccagaa tcccttcacg ctgttgaaga 600 ggaaaccgca gccggtgccc gcaggattgt tgccacctat tctaaggact tcttcgacgg 660 cgtcactttg atgtgcatgc tcggcgttga acctcagggc ctgcgttaca ccaaggtcgc 720

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_	gca Ala 230	_		-				-		_	_		_	_		1615
	cga Arg	_		-				_		_		-	_	_	~	1663
	gjà aaa															1711
	gag Glu															1759
	ggc Gly															1807
	gcg Ala 310															1855
	cgt Arg															1903
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ctg Leu	tat Tyr	acc Thr 375	gca Ala	gcc Ala	gat Asp	gtc Val	atg Met 380	ctg Leu	gtt Val	acg Thr	cct Pro	ttt Phe 385	Lys	gac Asp	ggt Gly	2047
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<213> Corynebacterium glutamicum

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Asp Met Thr Val His Pro Asp Gly Ser Tyr Ser Ile Ser Pro Ser Pro 20 25 30

Gly Gly Leu Val Thr Gly Leu Ser Pro Val Leu Glu Gln His Arg Gly

: ==

35 40 45

Cys	Trp	Val	Gly	Trp	Pro	Gly	Thr	Val	Asp	Val	Ala	Pro	Glu	Pro	Phe
	50					55					60				

- Arg Thr Asp Thr Gly Val Leu Leu His Pro Val Val Leu Thr Ala Ser 65 70 75 80
- Asp Tyr Glu Gly Phe Tyr Glu Gly Phe Ser Asn Ala Thr Leu Trp Pro 85 90 95
- Leu Phe His Asp Leu Ile Val Thr Pro Val Tyr Asn Thr Asp Trp Trp 100 105 110
- His Ala Phe Arg Glu Val Asn Leu Lys Phe Ala Glu Ala Val Ser Gln
 115 120 125
- Val Ala Ala His Gly Ala Thr Val Trp Val Gln Asp Tyr Gln Leu Leu 130 135 140
- Leu Val Pro Gly Ile Leu Arg Gln Met Arg Pro Asp Leu Lys Ile Gly 145 150 150
- Phe Phe Leu His Ile Pro Phe Pro Ser Pro Asp Leu Phe Arg Gln Leu 165 170 175
- Pro Trp Arg Glu Glu Ile Val Arg Gly Met Leu Gly Ala Asp Leu Val 180 185 190
- Gly Phe His Leu Val Gln Asn Ala Glu Asn Phe Leu Ala Leu Thr Gln 195 200 205
- Gln Val Ala Gly Thr Ala Gly Ser His Val Gly Gln Pro Asp Thr Leu 210 220
- Gln Val Ser Gly Glu Ala Leu Val Arg Glu Ile Gly Ala His Val Glu 225 $$ 230 $$ 235 $$ 240
- Thr Ala Asp Gly Arg Arg Val Ser Val Gly Ala Phe Pro Ile Ser Ile 245 250 255
- Asp Val Glu Met Phe Gly Glu Ala Ser Lys Ser Ala Val Leu Asp Leu 260 265 270

Leu Lys Thr Leu Asp Glu Pro Glu Thr Val Phe Leu Gly Val Asp Arg 275 280 285

Leu Asp Tyr Thr Lys Gly Ile Leu Gln Arg Leu Leu Ala Phe Glu Glu 290 295 300

Leu Leu Glu Ser Gly Ala Leu Glu Ala Asp Lys Ala Val Leu Leu Gln 305 310 315 320

Val Ala Thr Pro Ser Arg Glu Arg Ile Asp His Tyr Arg Val Ser Arg 325 330 335

Ser Gln Val Glu Glu Ala Val Gly Arg Ile Asn Gly Arg Phe Gly Arg 340 345 350

Met Gly Arg Pro Val Val His Tyr Leu His Arg Ser Leu Ser Lys Asn 355 360 365

Asp Leu Gln Val Leu Tyr Thr Ala Ala Asp Val Met Leu Val Thr Pro 370 375 380

Phe Lys Asp Gly Met Asn Leu Val Ala Lys Glu Phe Val Ala Asn His
385 390 395 400

Arg Asp Gly Thr Gly Ala Leu Val Leu Ser Glu Phe Ala Gly Ala Ala
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410
415

Thr Glu Leu Thr Gly Ala Tyr Leu Cys Asn Pro Phe Asp Val Glu Ser 420 425 430

Ile Lys Arg Gln Met Val Ala Ala Val His Asp Leu Lys His Asn Pro 435 440 445

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Ser Gly Glu Asn Ser 485

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